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GenCore version 4.5

protein search, using sw model

on: May 8, 2002, 11:08:00 ; Search time 28.8 Seconds
(without alignments)

2701.975 Million cell updates/sec

title: US-09-911-513-2

perfect score: 2758

sequence: 1 MKRDHHHHQDKTMMNNE.....MLGWHTRPLIATSAWKLSTN 532

scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

searched: 473505 seqs, 146272329 residues

total number of hits satisfying chosen parameters: 473505

minimum DB seq length: 0

maximum DB seq length: 2000000000

post-processing: Minimum Match 0%
Maximum Match 100%

RESULT	4			
023642	ID	PRELIMINARY;	PRT;	587 AA.
023642;	AC			
023642;	DT	01-JAN-1998 (TREMBLrel. 05, Created)		
	DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)		
	DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)		
	DE	RGAI PROTEIN.		
	GN	RGAI.		
OS		Arabidopsis thaliana (Mouse-ear cress).		
OC		Eukaryota; Viridiplantae; Streptophyta;		
OC		Spermatophyta; Magnoliophytes;		
OC		euurosids II; Brassicidae; Brassicaceae;		
OC		euurosids II; Brassicidae; Brassicaceae;		
OC		Arabidopsis; Arabidopsis; Arabidopsis s.		

[1] SEQUENCE FROM N.A. RP MEDLINE=91379310; RX Truong H.N., Caboche M., Daniel-Vedele F.; RA Sequence and characterization of two *Arabidopsis thaliana* cDNAs isolated by functional complementation of a yeast gln3 gdh1 mutant.; RT FEBS Lett. 410:213-218 (1997). RL EMBL: Y11336; CAA72477.1; DR Mendel: 24145; Arath: 30:51-24:45. DR SEQUENCE 587 AA; SQ D0A7A3C741FB51EF CRC64;

Query	Match	79	4%	Score	2189	5;	DB	10;	Length	587;
Best Local Similarity	74.5%	fred.	No. 5e-166;							
Matches	441;	Conservative	39;	Mismatches	43;	Indels	69;	Gaps		
Qy	1	MKRDHIIH	-----	-HH	-----	-----	-----	-----	-----	-----
Db	1	MKRDRHQQFQGRLLNQTSSSSS1SKDQKMMVKKREDGGNNMDLTDNPP	-----	-----	-----	-----	-----	-----	-----	-----
Qy	44	DVAQLEOLEYMSVNQEDDLISQLAETEYHNPAALEYTLDMSLT	-----	-----	-----	-----	-----	-----	-----	96
Db	61	EVALKLEOLETMMMSVNQEDCLSHLATAHTHYNPSELYSWIDNMSELNPPLPASSNGLD	-----	-----	-----	-----	-----	-----	-----	120
Qy	97	-----	-----	-----	-----	-----	-----	-----	AFYDLDKAIPGDAILNOFAIDSASSSSNOGGGGDTTYTNKRLK-CSN	140

QY	94	--SSNAYEYDLKAIP-----GDAIL-----NOFATDASSSSNNQQGGDT	129
Db	142	SVDSSSSYYALRPIPSAGATAPADLSAADSYRDPRKMRGGSSTSSSSSSSLGGG--	198
QY	130	YTNTNRKLCKNSNGVPIVE-----TTTAAESTRHVLYDQSENGVRVLHYHALLACAAYQKENL	184
Db	199	--ARSSVVAPPYAAANATPALEVVVDFTQE GIRL HALLACAAYQENL	250
QY	185	TVAEALVKIGFLAVSOIGAMRKVATYFAEALARIRYRL--SPSOSPIDHSLSLTQMFH	242
Db	251	SAAEALVKIQPIPLASQGGMRKVAAYEGERARVFRERFQDPSSLDAFDAJLHAFH	310
QY	243	YETCPYLUKFAHTANQAILEFGQKRRHVLFDSMSQGLOMPALMQLAALRPGGPVFRL	302
Db	311	YESCPLYLUKFAHTANQAILEFGQKRRHVYDFGKQGMQWPALIQLAALRPGGPSFRL	370
QY	303	TGIGPAPDNFDLYHEVGCKLHLAHABAHYHEFGRFGVANTLADLEPFMLQPEGEDPNE	430
Db	371	TGVGPPDDEDAQQYQWKLQAFATTIRYDFQYQLVAATLADLEPFMLQPEGEDPNE	430
QY	358	EYESAVVNSYFELHKLLGRPGAIKDVKYLGVVYQNIKEPEIIFTYVEQESNNHNSPTIFLDRTESL	417
Db	431	EPEVIAVNSVEMHRLLAQPGALEKVLYGTIVRAVRSPRIVTEQEANHNSCTFELDRTESL	490
QY	418	HYYSTLEDSLQ-----VPSGQDKVMSEVYLGKQICNVAQACGPDRY	459
Db	491	HYYSTWEDSLEGGSGGGPSEVSSGAAAAPAAGTQDVNSEVYLGKQICNVAQEGAERT	550
QY	460	ERHETLSQWRNRFGSAGFAAHIGNSNAFKQASMLALFNGEGYRVEESPQCLMIGWHTR	519
Db	551	ERHETLGQWRNLNLGNAGFETVHLGSNAYKOASTLIALFAGGDGTKEEKGLTIGWHTR	610
QY	520	PLIATSAWKLS	530
Db	611	PLIATSAWLRA	621
RESULT 10			
Q9C8Y3	PRELIMINARY;	PRT;	511 AA.
ID			
AC	Q9C8Y3		
DT	01-JUN-2001 (TREMBLrel. 17, Created)		
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)		
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)		
DE	GIBBERELLIN REGULATORY PROTEIN, PUTATIVE.		
GN	T27F4.10.		
OS	Arabidopsis thaliana (Mouse-ear cress).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;		
OC	eurosioides II; Brassicales; Brassicaceae; Arabidopsis.		
NCBI_TAXID	=1702;		
RN	[1]		
SEQUENCE FROM N.A.			
RP	STRAIN/CCV, COLUMBIA;		
RX	MEDLINE=21016719; PubMed=11130712;		
RA	Theologis A., Ecker J.R., Palm C.J., Fedderspiel N.A., Kaul S.,		
RA	White O., Alonso J., AltAfri H., Arsujo R., Bowman C.L., Brocks S.Y.,		
RA	Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,		
RA	Chung M.K., Conn J., Conway A.R., Dewar K.,		
RA	Dunn P., Engu P., Fieldblum T.Y., Feng J.-D., Fong B., Fujii Y., Huizar L.,		
RA	Gill J.E., Goldsmith A.D., Haas B., Hansens N.P., Hughes B., Khaykin E.,		
RA	Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Kremenetskaya I., Kurtz D.B., Lam B.,		
RA	Kim C.J., Koo H.I., Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,		
RA	Liu X., Liu S.X., Liu Z.A., Lueros J.S., Maiti R., Marziali A.,		
RA	Millettier J., Miranda A., Nguyen M., Nierman W.C., Osborne B.I.,		
RA	Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,		
RA	Sakano H., Salziger S.L., Schwatz J.R., Shinn P., Southwick A.M.,		
RA	Sun H., Tam L.J., Tambunga G., Toriumi M.J., Town C.D., Utterback T., van Aken S., Vaysberg M., Vysotskaya V.S., Walker M.,		
RA	Wu D., Yu G., Fraser C.M., Venier J.C., Davis R.W.;		
RT	"Sequence and analysis of chromosome 1 of the plant Arabidopsis thaliana."		

DR EMBL; AC009895; AAF01590.1; -					
SEQUENCE 547 AA; 60493 MW; C4D18D5951D95634 CRC64;					
Query Match 56.3%; Score 1552.5; DB 10; Length 547;					
Best Local Similarity 59.0%; Pred. No. 4.5e-111;					
Matches 323; Conservative 79; Mismatches 90; Indels 55; Gaps 13;					
Query Match 56.3%; Score 1552.5; DB 10; Length 547;					
Best Local Similarity 59.0%; Pred. No. 4.5e-111;					
Matches 323; Conservative 79; Mismatches 90; Indels 55; Gaps 13;					
Qy 11 DKTTMMNEEDGNGM ---DELLAVLGKYKVRSSSEMDAYAQKLEQEYMMNSVQEDDL SQ 66					
Db 29 DKK--- KADDNNNSNNMDDELLAVLGKYKVRSSSEMDAYAQKLEQEYMMNSVQEDDL SQ 66					
Qy 67 LATETVHNPAAELYTLWSDMLTDLNPPSSN-----AEYDLKAIPGDAILNQF - 113					
Db 82 VLNDSVHYNPSDLSNWESMLSELNNPASDLDTRSCVDSEYDLRAIPG---LSAfk 138					
Qy 114 --AIDSASSSNNGGGDTYTNNKRLCSNGVYVETTATAESTRVHVLDSOENGVRVLYH 170					
Db 139 EEEVFDEPSS-----KRIRGS---WCESDESPrSVLVDQSQTGVRLH 182					
Qy 171 ALLACAAVQKENLTVAEALVKQIGFLAVSQIGAMRKVATYFAFALARRYRSLPSQ - 227					
Db 183 ALVACAAEATHQENLNLA DALVLRKGTLAGSQAGMKVATYFAQALARRYRDLTAETDV 242					
Qy 228 -SPIDHSLSDTLOMHFETCPYLKAIPGDAILNQ 112					
Db 243 CAAVNPSFEVLEMHEYSCPVYKFAIETANQIALEAVTTARVHVIDGLNGMQWPL 302					
Qy 287 MOALALRPGGPVFRLTGIGPAPDNFDLYHEVGCKLHLAAEAIHVEPEYRGFVANTLAD 346					
Db 303 MOALALRPGGPSFRUJGIGPOTENSSLQOQGWKLQAFAQQMGVVEFKGAESLSD 362					
Qy 347 LDASMELRPSLELESVAVNSVPELHKLGRPAIDKVILGVGVNOIKPELFVYEQESNHN 406					
Db 363 LEPEMFTRP-ESETLVVNSVPELHRLJARSGSIEKLUNTVRAIKPSLVTVQEANING 421					
Qy 407 PFIELDRTESLHYYSTLDSLSE --GYPSGDQKYMSEVYLGRQICMVVAQGDPRVERHE 463					
Db 422 IVFLDRNEAHYSSLEFDLSLSDSYLPS-QDRVMSEYLVGRQILNVAAEGSDRVERHE 480					
Qy 464 TLSQWRNRFGSAGFAAAHGSNAFKOASMLLALFGNGGEYREBESDGLCLMGLHTRPLI 523					
Db 481 TAAQWRTRMSAGFDPIHLSASSFKQASMLLSLYATGDDYRVEENDGLMIGNQTRPLI 540					
Qy 524 TSAWKLS 530					
Db 541 TSAWKL A 547					
RESULT 13					
Q9LF53 PRELIMINARY; PRIT; 523 AA.					
ID Q9LF53 PRELIMINARY; PRIT; 523 AA.					
AC Q9LF53; PRELIMINARY; PRIT; 523 AA.					
DT 01-OCT-2000 (TREMBLrel. 15, Created)					
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)					
DE RGA-LIKE PROTEIN.					
GN K3M16_60.					
OS Arabidopsis thaliana (Mouse-ear cress).					
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;					
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.					
OX NCBI_TAXID=3702;					
RN [1]					
RP SEQUENCE FROM N.A.					
RA RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Kotani H.,					
RA RA Tabata S., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;					
RA RA EU Arabidopsis sequencing project;					
RA RA Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.					
RL [2]					
RN SEQUENCE FROM N.A.					
STRAIN_CV: COLUMBIA;					
Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,					
Bowman C.L., White O., Nierman W.C., Fraser C.M.,					
"Arabidopsis thaliana" chromosome III BAC 21P5 genomic sequence.;					
Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.					
RN [1]					
RP SEQUENCE FROM N.A.					
RA RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Kotani H.,					
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Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,					
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RA RA Tabata S., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;					
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RA RA Tabata S., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;					
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RA RA Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.					
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Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,					
Bowman C.L., White O., Nierman W.C., Fraser C.M.,					
"Arabidopsis thaliana" chromosome III BAC 21P5 genomic sequence.;					
Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.					
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RA RA Tabata S., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;					
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RA RA Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.					
RL [2]					
RN SEQUENCE FROM N.A.					
STRAIN_CV: COLUMBIA;					
Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,					
Bowman C.L., White O., Nierman W.C., Fraser C.M.,					
"Arabidopsis thaliana" chromosome III BAC 21P5 genomic sequence.;					
Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.					
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RA RA Tabata S., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;					
RA RA EU Arabidopsis sequencing project;					
RA RA Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.					
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STRAIN_CV: COLUMBIA;					
Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,					
Bowman C.L., White O., Nierman W.C., Fraser C.M.,					
"Arabidopsis thaliana" chromosome III BAC 21P5 genomic sequence.;					
Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.					
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RP SEQUENCE FROM N.A.					
RA RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Kotani H.,					
RA RA Tabata S., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;					
RA RA EU Arabidopsis sequencing project;					
RA RA Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.					
RL [2]					
RN SEQUENCE FROM N.A.					
STRAIN_CV: COLUMBIA;					
Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,					
Bowman C.L., White O., Nierman W.C., Fraser C.M.,					
"Arabidopsis thaliana" chromosome III BAC					

SQ	SEQUENCE	523 AA;	57326 MW;	0F6CE0BD13403C35 CRC64;	
Query Match					
Best Local Similarity	54.0%	Score 1490; DB 10;	Length 523;		
Matches	315;	Pred. No. 2.7e-106;	Mismatches 78;	Indels 52;	Gaps 14;
Matches	194;	Conservative 63;	Mismatches 101;	Indels 15;	Gaps 7;
Db	1 MKRSHQETSYEEA\$MVKELENCGGGGDDNMDEFLEVLYKVRSSDMADVAKLEOLE	53			
Qy	1 : : : : : : : : : :				
Db	1 MKRSHQETSYEEA\$MVKELENCGGGGDDNMDEFLEVLYKVRSSDMADVAKLEOLE	60			
Qy	54 VMMSNYQEDDL---SQQATEVHNPAELYWLDSMLTDIN---PPSSNAEYDIAPIED	107			
Db	61 MVLSN---DIASSSNAFNDTWHNPSDSLGSWASQMSLSDLNYYPDLPNRICDLRPTDD	116			
Qy	108 AILNOFAIDSASSNSNQGGGDTTYTNKRK---CSNGVTTETATAESTRHVLVDSE	163			
Db	117 ------DECSSNS-----NSNKRIKLGPNCD-----SVTSESTRSVLI--BE	152			
Qy	164 NGVRVHALLACAENA\$VKENUTVAELVKOIGFLAVSQIGMVKVATYFAEALARRIYR	223			
Db	153 TGVRLYQALVACAEA\$VQLENISLADALVERGLLIAASQAGMVKVATYFAEALARRIY	212			
Qy	224 SPQSOPIDHSLSLSDTQMHFYTCPYLKFAHTANOAILEAFQGKQKRVHVIDSMSQGLOW	283			
Db	213 HPSAAAIDPSPFEETLQMFNTDSCPLKFAHTANQAILEAVTTSRVVHIDLGINOGHGW	272			
Qy	284 PALMODALRPGGPVFRLLTGIPAPDNDYLHVGCKKAHLAETHA\$VBFYEFYRGFVANT	343			
Db	273 PALMODALRPGGPSPRLTGVGNPS--NREGIQELGWKLQLAQAGVEFKGLTTER	330			
Qy	344 LADLDASMLLRPSPTEVASVNSYFELHKLGRPSAIDKVLGVYNNQIKPBEIFTVEQESN	403			
Db	331 LSDLDLDMFTR-RESETLVNSYFELHVLSQPSISIEKATYKAVKGVLVIVQEAN	389			
Qy	404 HNSPIFLDRETESLHYYSTLFDLSLEG--VPSGDQKVNSEVYLGKQICNVACDGPDVE	460			
Db	390 HNGFLDRENEALHYSSSLFDLSLEDGVVPS-ODRMVSEVYLGRQILNLVATEGSDRIE	448			
Qy	461 RHETLSQWRNRFSGAGFAAHIGSNAPKAOSMLALFNGEGTVVEESQCLMGLWHTRP	520			
Db	449 RHETLAQWRNRMGSAGFDPYNLGSDAFKQASLILLALSGGGDGYRVEENDGSLMLAWQTKP	508			
Qy	521 LIATSAWKLS 530				
Db	509 LIASAWKLA 518				
RESULT 14					
Q9AS97		PRELIMINARY;	PRT;	493 AA.	
ID	Q9AS97				
AC					
DT	01-JUN-2001 (TREMBLrel. 17, Created)				
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)				
DE	PUTATIVE OSGAI.				
GN	P0707D10_30.				
OS	Oryza sativa (Rice).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
CC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;				
EC	Ehrhartoideae; Poales; Poaceae;				
NCBI_TAXID=4530;					
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CV. ALASKA;				
RA	Sassa N., Matsushita Y., Nakamura T., Nyunoya H.;				
RT	"Molecular characterization and in situ expression pattern of pea SCARICROW gene."				
RT	Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.				
RL	EMBL; AB048113; BAB31955.1;				
DR	SEQUENCE - 819 AA; 90372 MW;				
SQ	41B67BD6DC72ADFA CRC64;				
Query Match					
Best Local Similarity	35.1%	Score 967.5;	DB 10;	Length 493;	
Matches	194;	Conservative 63;	Mismatches 101;	Indels 15;	Gaps 7;
Db	165 GVRVHALLACAENA\$VKENUTVAELVALV - KQIGFLAVSQIGMVKVATYFAEALARRIY-	221			
Qy	81 GIRLVHLLNSCAGAEAGDHALASAQLADSHAALA\$AAASGIGRVA\$VFTTALSRRLF	140			
Db	222 -RLSPSQSPIDHSLSLSDTQMHFYTCPYLKFAHTANQAILEAFQGKRVHVIDSMSQG	280			
Qy	141 SPVAPPTDAAEHAF--LTHFYEAZCPYLKFAHTANQAILEAHFGCHVHVIDFSLM	197			
Db	281 LQWPALMQAIALRPGGPYPERLTGTGPPAPDNFDLYHEVCKLAHLAETHA\$VFTYGRFV	340			
Qy	198 LQWPALQIAALRPGGPSPRITGPPSPGSPTRDGLRGLADLARSVRVRSFRGV	257			
Db	341 ANTЛАДА\$МЛЕРРСЕІЕ\$ВА\$Н\$ФЕЛ\$ХЛ\$ГРР--\$АИД\$К\$Л\$Г\$В\$Н\$О\$И\$К\$П\$Е\$И\$Т\$	397			
Qy	258 AN\$Л\$Д\$В\$Р\$М\$Л\$О\$А\$Р\$--\$Е\$А\$В\$Ф\$Н\$В\$Л\$О\$Л\$Г\$Д\$П\$А\$Д\$О\$	315			
Db	398 VEQENHNSP\$IFL\$D\$T\$E\$Л\$H\$Y\$S\$T\$L\$F\$D\$S\$L\$E\$G\$V\$P\$--\$G\$D\$K\$У\$M\$E\$V\$Y\$Л\$G\$K\$O\$C\$N\$V\$A\$C\$D\$G\$	455			
Qy	316 TEQEDAHNTKGELD\$T\$E\$А\$Л\$F\$Y\$S\$A\$V\$E\$D\$U\$D\$A\$A\$A\$S\$G\$G\$A\$N\$A\$M\$A\$E\$A\$Y\$L\$O\$R\$M\$Y\$G\$F\$S\$--\$G\$E\$H\$S\$Y\$E\$A\$D\$G\$C\$T\$L\$G\$	375			
Db	376 A\$R\$B\$R\$H\$E\$P\$LS\$W\$R\$D\$R\$L\$T\$R\$A\$G\$S\$A\$V\$P\$G\$S\$N\$A\$L\$Q\$A\$R\$M\$Y\$G\$F\$S\$--\$G\$E\$H\$S\$Y\$E\$A\$D\$G\$C\$T\$L\$G\$	434			
Qy	516 WHTREPLIATSAWK 528				
Db	435 WHGRPLFSA\$AWE 447				
RESULT 15					
Q9AVK4		PRELIMINARY;	PRT;	819 AA.	
ID	Q9AVK4				
AC	Q9AVK4;				
DT	01-JUN-2001 (TREMBLrel. 17, Created)				
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)				
DE	SCARICROW.				
GN	PSSCR.				
OS	Pisum sativum (Garden pea).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	euroids I; Fabales; Fabaceae; Papilionoideae; Pisum.				
OX	NCBI_TaxID=3888;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CV. ALASKA;				
RA	Sassa N., Matsushita Y., Nakamura T., Nyunoya H.;				
RT	"Molecular characterization and in situ expression pattern of pea SCARICROW gene."				
RT	Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.				
RL	EMBL; AB048113; BAB31955.1;				
DR	SEQUENCE - 819 AA; 90372 MW;				
SQ	41B67BD6DC72ADFA CRC64;				
Query Match					
Best Local Similarity	22.1%	Score 608.5;	DB 10;	Length 819;	
Matches	168;	Conservative 38;	Mismatches 87;	Indels 67;	Gaps 19;
Db	53 EVMM\$N\$Q\$E\$D\$S\$Q\$A\$T\$E\$V\$H\$N\$P\$A\$E\$Y\$T\$W\$D\$S\$M\$T\$D\$N\$P\$S\$N\$A\$E\$Y\$D\$K\$A\$P\$G\$D\$A\$--\$109				
Qy	344 DV\$P\$T\$H\$E\$D\$S\$T\$L\$N\$Q\$N\$Q\$N\$--\$M\$P\$W\$G\$A\$T\$Q\$N\$N\$N\$P\$S\$--\$V\$S\$V\$T\$L\$P\$Q\$P\$S\$T\$Q\$	397			
Db	110 -----LNQFAIDSASSNSNQGGGDTTYTNKRLKCNSG\$V\$ET\$T\$A\$E\$T\$R\$H\$V\$L\$V\$D\$Q\$-	162			
Qy	398 QDQOHQOH\$P\$E\$D\$A\$P\$T\$--\$T\$T\$T\$A\$E\$L\$--\$A\$L\$A\$R\$K\$K\$E\$E\$Q\$K\$K\$K\$4\$4\$0				
Db	441 DEEGLHLTLLOCAEAVSAENLEQANKMLEISOL\$P\$T\$F\$G\$T\$A\$Q\$V\$A\$Y\$F\$E\$A\$N\$A\$R\$V\$	500			

Qy	220	- - - - - TYRLSP - - SQSPLDHSLSLDTQLMHF YETCPYLKFAHETANQAILEAFQGKRVHV	272
Db	501	SSCLGIATLPYSSHTPHNQKVASYAFCV- FNGISPPVKFSEHTANQAIEAFERERVHI	559
Qy	273	IDFSMSGLQWPALMOMALRPGGPYFRLIGPPADPNDFLYEVGCKLAHLAAIHV	332
Db	560	IDLDMQGLONGLFLHTASREGGPYVRLTG --- TSMETLEATGKRLSDFFANKLGL	615
Qy	333	EPEYRGF - VANTLADLDASMELPRLPSSEAVNSVFELHLGLRPGDAIDKVLGVNQIK	391
Db	616	PPEF - - PVAEKVGNDIVEKLNV - - SKSEAYAH - - WLQHSLYDYGSDINTNLWLQLRA	669
Qy	392	PEIIFTVVQEHNNSPFLDLRFTESLHYSTLFDSL - - EGVPSGODKVMSEVYLQKQIC	448
Db	670	PKVVTVVEQDLS - NAGSFLGRFEVAAHYSAFLDSLGSSYGESEERHVVYEQQLSREIR	728
Qy	449	NVACDGPDR - - VERHETLISQWRNRFGSAGFAAAHGSNAFKOASMLLAFNGGEGYRV	505
Db	729	NVLAVGGPSRSGEIKFH - - NWREKLQQCGRGVSLAGNAATQASLLGMF - PSEGVTYI	783
Qy	506	EEDGCLMLGWHTRPLJATSAWK	528
Db	784	VEDNGTILKGLKWDCLCLITASAWR	806

search completed: May 8, 2002, 11:11:32
Job time: 212 sec

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